SEQUENCE LISTING

<110> Tavtigian, Sean V.
      Teng, David H.F.
      Simard, Jacques
      Rommens, Johanna M.
      Myriad Genetics, Inc.

<120> Chromosome 17q-Linked Prostate Cancer Susceptibility
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<150> US 60/107,468
<151> 1999-11-06

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<170> PatentIn Ver. 2.0

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tcg cag gga cgc acc ata tcg cag gca ccc gcc cgc cgc gag cgg ccg   96
Ser Gln Gly Arg Thr Ile Ser Gln Ala Pro Ala Arg Arg Glu Arg Pro
                20   25   30

cgc aag gac ccg ctg cgg cac ctg cgc acg cga gag aag cgc gga ccg   144
Arg Lys Asp Pro Leu Arg His Leu Arg Thr Arg Glu Lys Arg Gly Pro
            35   40   45

tcg ggg tgc tcc ggc ggc cca aac acc gtg tac ctg cag gtg gtg gca   192
Ser Gly Cys Ser Gly Gly Pro Asn Thr Val Tyr Leu Gln Val Val Ala
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gcg ggt agc cgg gac tcg ggc gcc gcg ctc tac gtc ttc tcc gag ttc   240
Ala Gly Ser Arg Asp Ser Gly Ala Ala Leu Tyr Val Phe Ser Glu Phe
65   70   75   80

aac cgg tat ctc ttc aac tgt gga gaa ggc gtt cag aga ctc atg cag   288
Asn Arg Tyr Leu Phe Asn Cys Gly Glu Gly Val Gln Arg Leu Met Gln
                85   90   95

gag cac aag tta aag gtt gct cgc ctg gac aac ata ttc ctg aca cga   336
Glu His Lys Leu Lys Val Ala Arg Leu Asp Asn Ile Phe Leu Thr Arg
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atg cac tgg tct aat gtt ggg ggc tta agt gga atg att ctt act tta    384
Met His Trp Ser Asn Val Gly Gly Leu Ser Gly Met Ile Leu Thr Leu
        115             120             125

aag gaa acc ggg ctt cca aag tgt gta ctt tct gga cct cca caa ctg    432
Lys Glu Thr Gly Leu Pro Lys Cys Val Leu Ser Gly Pro Pro Gln Leu
        130             135             140

gaa aaa tac ctc gaa gca atc aaa ata ttt tct ggt cca ttg aaa gga    480
Glu Lys Tyr Leu Glu Ala Ile Lys Ile Phe Ser Gly Pro Leu Lys Gly
145             150             155             160

ata gaa ctg gct gtg cgg ccc cac tct gcc cca gaa tac gag gat gaa    528
Ile Glu Leu Ala Val Arg Pro His Ser Ala Pro Glu Tyr Glu Asp Glu
                165             170             175

acc atg aca gtt tac cag atc ccc ata cac agt gaa cag agg agg gga    576
Thr Met Thr Val Tyr Gln Ile Pro Ile His Ser Glu Gln Arg Arg Gly
            180             185             190

aag cac caa cca tgg cag agt cca gaa agg cct ctc agc agg ctc agt    624
Lys His Gln Pro Trp Gln Ser Pro Glu Arg Pro Leu Ser Arg Leu Ser
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cca gag cga tct tca gac tcc gag tcg aat gaa aat gag cca cac ctt    672
Pro Glu Arg Ser Ser Asp Ser Glu Ser Asn Glu Asn Glu Pro His Leu
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cca cat ggt gtt agc cag aga aga ggg gtc agg gac tct tcc ctg gtc    720
Pro His Gly Val Ser Gln Arg Arg Gly Val Arg Asp Ser Ser Leu Val
225             230             235             240

gta gct ttc atc tgt aag ctt cac tta aag aga gga aac ttc ttg gtg    768
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                245             250             255

ctc aaa gca aag gag atg ggc ctc cca gtt ggg aca gct gcc atc gct    816
Leu Lys Ala Lys Glu Met Gly Leu Pro Val Gly Thr Ala Ala Ile Ala
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ccc atc att gct gct gtc aag gac ggg aaa agc atc act cat gaa gga    864
Pro Ile Ile Ala Ala Val Lys Asp Gly Lys Ser Ile Thr His Glu Gly
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aga gag att ttg gct gaa gag ctg tgt act cct cca gat cct ggt gct    912
Arg Glu Ile Leu Ala Glu Glu Leu Cys Thr Pro Pro Asp Pro Gly Ala
        290             295             300

gct ttt gtg gtg gta gaa tgt cca gat gaa agc ttc att caa ccc atc    960
Ala Phe Val Val Val Glu Cys Pro Asp Glu Ser Phe Ile Gln Pro Ile
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tgt gag aat gcc acc ttt cag agg tac caa gga aag gca gat gcc ccc   1008
Cys Glu Asn Ala Thr Phe Gln Arg Tyr Gln Gly Lys Ala Asp Ala Pro
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gtg gcc ttg gtg gtt cac atg gcc cca gca tct gtg ctt gtg gac agc   1056
Val Ala Leu Val Val His Met Ala Pro Ala Ser Val Leu Val Asp Ser
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gtc ctg aat gag aac tgt gcc tca gtt cac aac ctt cgc agc cac aag   1152
Val Leu Asn Glu Asn Cys Ala Ser Val His Asn Leu Arg Ser His Lys
        370                 375                 380

att caa acc cag ctc aac ctc atc cac ccg gac atc ttc ccc ctg ctc   1200
Ile Gln Thr Gln Leu Asn Leu Ile His Pro Asp Ile Phe Pro Leu Leu
385                 390                 395                 400

acc agt ttc cgc tgt aag aag gag ggc ccc acc ctc agt gtg ccc atg   1248
Thr Ser Phe Arg Cys Lys Lys Glu Gly Pro Thr Leu Ser Val Pro Met
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gtt cag ggt gaa tgc ctc ctc aag tac cag ctc cgt ccc agg agg gag   1296
Val Gln Gly Glu Cys Leu Leu Lys Tyr Gln Leu Arg Pro Arg Arg Glu
            420                 425                 430

tgg cag agg gat gcc att att act tgc aat cct gag gaa ttc ata gtt   1344
Trp Gln Arg Asp Ala Ile Ile Thr Cys Asn Pro Glu Glu Phe Ile Val
        435                 440                 445

gag gcg ctg cag ctt ccc aac ttc cag cag agc gtg cag gag tac agg   1392
Glu Ala Leu Gln Leu Pro Asn Phe Gln Gln Ser Val Gln Glu Tyr Arg
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agg agt gcg cag gac ggc cca gcc cca gca gag aaa aga agt cag tac   1440
Arg Ser Ala Gln Asp Gly Pro Ala Pro Ala Glu Lys Arg Ser Gln Tyr
465                 470                 475                 480

cca gaa atc atc ttc ctt gga aca ggg tct gcc atc ccg atg aag att   1488
Pro Glu Ile Ile Phe Leu Gly Thr Gly Ser Ala Ile Pro Met Lys Ile
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cga aat gtc agt gcc aca ctt gtc aac ata agc ccc gac acg tct ctg   1536
Arg Asn Val Ser Ala Thr Leu Val Asn Ile Ser Pro Asp Thr Ser Leu
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cta ctg gac tgt ggt gag ggc aca ttt ggg cag ctg tgc cgt cat tac   1584
Leu Leu Asp Cys Gly Glu Gly Thr Phe Gly Gln Leu Cys Arg His Tyr
            515                 520                 525

gga gac cag gtg gac agg gtc ctg ggc acc ctg gct gct gtg ttt gtg   1632
Gly Asp Gln Val Asp Arg Val Leu Gly Thr Leu Ala Ala Val Phe Val
        530                 535                 540

tcc cac ctg cac gca gat cac cac acg ggc ttg cca agt atc ttg ctg   1680
Ser His Leu His Ala Asp His His Thr Gly Leu Pro Ser Ile Leu Leu
545                 550                 555                 560

cag aga gaa cgc gcc ttg gca tct ttg gga aag ccg ctt cac cct ttg   1728
Gln Arg Glu Arg Ala Leu Ala Ser Leu Gly Lys Pro Leu His Pro Leu
                565                 570                 575

ctg gtg gtt gcc ccc aac cag ctc aaa gcc tgg ctc cag cag tac cac   1776
Leu Val Val Ala Pro Asn Gln Leu Lys Ala Trp Leu Gln Gln Tyr His
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aac cag tgc cag gag gtc ctg cac cac atc agt atg att cct gcc aaa      1824
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tgc ctt cag gaa ggg gct gag atc tcc agt cct gca gtg gaa aga ttg      1872
Cys Leu Gln Glu Gly Ala Glu Ile Ser Ser Pro Ala Val Glu Arg Leu
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atc agt tcg ctg ttg cga aca tgt gat ttg gaa gag ttt cag acc tgt      1920
Ile Ser Ser Leu Leu Arg Thr Cys Asp Leu Glu Glu Phe Gln Thr Cys
625                 630             635                 640

ctg gtg cgg cac tgc aag cat gcg ttt ggc tgt gcg ctg gtg cac acc      1968
Leu Val Arg His Cys Lys His Ala Phe Gly Cys Ala Leu Val His Thr
                645             650                 655

tct ggc tgg aaa gtg gtc tat tcc ggg gac acc atg ccc tgc gag gct      2016
Ser Gly Trp Lys Val Val Tyr Ser Gly Asp Thr Met Pro Cys Glu Ala
                660             665             670

ctg gtc cgg atg ggg aaa gat gcc acc ctc ctg ata cat gaa gcc acc      2064
Leu Val Arg Met Gly Lys Asp Ala Thr Leu Leu Ile His Glu Ala Thr
            675             680             685

ctg gaa gat ggt ttg gaa gag gaa gca gtg gaa aag aca cac agc aca      2112
Leu Glu Asp Gly Leu Glu Glu Glu Ala Val Glu Lys Thr His Ser Thr
        690             695             700

acg tcc caa gcc atc agc gtg ggg atg cgg atg aac gcg gag ttc att      2160
Thr Ser Gln Ala Ile Ser Val Gly Met Arg Met Asn Ala Glu Phe Ile
705                 710             715                 720

atg ctg aac cac ttc agc cag cgc tat gcc aag gtc ccc ctc ttc agc      2208
Met Leu Asn His Phe Ser Gln Arg Tyr Ala Lys Val Pro Leu Phe Ser
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ccc aac ttc agc gag aaa gtg gga gtt gcc ttt gac cac atg aag gtc      2256
Pro Asn Phe Ser Glu Lys Val Gly Val Ala Phe Asp His Met Lys Val
            740             745             750

tgc ttt gga gac ttt cca aca atg ccc aag ctg att ccc cca ctg aaa      2304
Cys Phe Gly Asp Phe Pro Thr Met Pro Lys Leu Ile Pro Pro Leu Lys
            755             760             765

gcc ctg ttt gct ggc gac atc gag gag atg gag gag cgc agg gag aag      2352
Ala Leu Phe Ala Gly Asp Ile Glu Glu Met Glu Glu Arg Arg Glu Lys
        770             775             780

cgg gag ctg cgg cag gtg cgg gcg gcc ctc ctg tcc agg gag ctg gca      2400
Arg Glu Leu Arg Gln Val Arg Ala Ala Leu Leu Ser Arg Glu Leu Ala
785                 790             795                 800

ggc ggc ctg gag gat ggg gag cct cag cag aag cgg gcc cac aca gag      2448
Gly Gly Leu Glu Asp Gly Glu Pro Gln Gln Lys Arg Ala His Thr Glu
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gag cca cag gcc aag aag gtc aga gcc cag tga                          2481
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Arg Lys Asp Pro Leu Arg His Leu Arg Thr Arg Glu Lys Arg Gly Pro
            35                  40                  45

Ser Gly Cys Ser Gly Gly Pro Asn Thr Val Tyr Leu Gln Val Val Ala
        50                  55                  60

Ala Gly Ser Arg Asp Ser Gly Ala Ala Leu Tyr Val Phe Ser Glu Phe
 65                  70                  75                  80

Asn Arg Tyr Leu Phe Asn Cys Gly Glu Gly Val Gln Arg Leu Met Gln
                85                  90                  95

Glu His Lys Leu Lys Val Ala Arg Leu Asp Asn Ile Phe Leu Thr Arg
            100                 105                 110

Met His Trp Ser Asn Val Gly Gly Leu Ser Gly Met Ile Leu Thr Leu
            115                 120                 125

Lys Glu Thr Gly Leu Pro Lys Cys Val Leu Ser Gly Pro Pro Gln Leu
            130                 135                 140

Glu Lys Tyr Leu Glu Ala Ile Lys Ile Phe Ser Gly Pro Leu Lys Gly
145                 150                 155                 160

Ile Glu Leu Ala Val Arg Pro His Ser Ala Pro Glu Tyr Glu Asp Glu
                165                 170                 175

Thr Met Thr Val Tyr Gln Ile Pro Ile His Ser Glu Gln Arg Arg Gly
            180                 185                 190

Lys His Gln Pro Trp Gln Ser Pro Glu Arg Pro Leu Ser Arg Leu Ser
            195                 200                 205

Pro Glu Arg Ser Ser Asp Ser Glu Ser Asn Glu Asn Glu Pro His Leu
            210                 215                 220

Pro His Gly Val Ser Gln Arg Arg Gly Val Arg Asp Ser Ser Leu Val
225                 230                 235                 240

Val Ala Phe Ile Cys Lys Leu His Leu Lys Arg Gly Asn Phe Leu Val
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Leu Lys Ala Lys Glu Met Gly Leu Pro Val Gly Thr Ala Ala Ile Ala
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Pro Ile Ile Ala Ala Val Lys Asp Gly Lys Ser Ile Thr His Glu Gly
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Val Ala Leu Val Val His Met Ala Pro Ala Ser Val Leu Val Asp Ser
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Arg Tyr Gln Gln Trp Met Glu Arg Phe Gly Pro Asp Thr Gln His Leu
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Val Leu Asn Glu Asn Cys Ala Ser Val His Asn Leu Arg Ser His Lys
    370                 375                 380

Ile Gln Thr Gln Leu Asn Leu Ile His Pro Asp Ile Phe Pro Leu Leu
385                 390                 395                 400

Thr Ser Phe Arg Cys Lys Lys Glu Gly Pro Thr Leu Ser Val Pro Met
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Val Gln Gly Glu Cys Leu Leu Lys Tyr Gln Leu Arg Pro Arg Arg Glu
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Trp Gln Arg Asp Ala Ile Ile Thr Cys Asn Pro Glu Glu Phe Ile Val
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Glu Ala Leu Gln Leu Pro Asn Phe Gln Gln Ser Val Gln Glu Tyr Arg
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Arg Ser Ala Gln Asp Gly Pro Ala Pro Ala Glu Lys Arg Ser Gln Tyr
465                 470                 475                 480

Pro Glu Ile Ile Phe Leu Gly Thr Gly Ser Ala Ile Pro Met Lys Ile
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Leu Leu Asp Cys Gly Glu Gly Thr Phe Gly Gln Leu Cys Arg His Tyr
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Gly Asp Gln Val Asp Arg Val Leu Gly Thr Leu Ala Ala Val Phe Val
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Ser His Leu His Ala Asp His His Thr Gly Leu Pro Ser Ile Leu Leu
545                 550                 555                 560

Gln Arg Glu Arg Ala Leu Ala Ser Leu Gly Lys Pro Leu His Pro Leu
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      Leu Val Arg His Cys Lys His Ala Phe Gly Cys Ala Leu Val His Thr
                      645                 650                 655

      Ser Gly Trp Lys Val Val Tyr Ser Gly Asp Thr Met Pro Cys Glu Ala
                  660                 665                 670

      Leu Val Arg Met Gly Lys Asp Ala Thr Leu Leu Ile His Glu Ala Thr
                  675                 680                 685

      Leu Glu Asp Gly Leu Glu Glu Glu Ala Val Glu Lys Thr His Ser Thr
          690                 695                 700

      Thr Ser Gln Ala Ile Ser Val Gly Met Arg Met Asn Ala Glu Phe Ile
      705                 710                 715                 720

      Met Leu Asn His Phe Ser Gln Arg Tyr Ala Lys Val Pro Leu Phe Ser
                      725                 730                 735

      Pro Asn Phe Ser Glu Lys Val Gly Val Ala Phe Asp His Met Lys Val
                  740                 745                 750

      Cys Phe Gly Asp Phe Pro Thr Met Pro Lys Leu Ile Pro Pro Leu Lys
                  755                 760                 765

      Ala Leu Phe Ala Gly Asp Ile Glu Glu Met Glu Glu Arg Arg Glu Lys
          770                 775                 780

      Arg Glu Leu Arg Gln Val Arg Ala Ala Leu Leu Ser Arg Glu Leu Ala
      785                 790                 795                 800

      Gly Gly Leu Glu Asp Gly Glu Pro Gln Gln Lys Arg Ala His Thr Glu
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<222> (1)..(113)
<223> exon 11

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<212> DNA
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<222> (1)..(96)
<223> exon 12

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<212> DNA
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<223> exon 13

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<210> 28
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      8186-8244; exon 9: 12878-12936; exon 10:
      13032-13104;

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<222> (13756)..(22917)
<223> exon 11: 13756-13868; exon 12: 15283-15378; exon
      13: 16278-16416; exon 14: 16498-16583; exon 15:
      18583-18701; exon 16: 20349-20445; exon 17:
      22172-22310; exon 18: 22879-22917

<220>
<221> misc_feature
<222> (23045)..(26452)
<223> exon 19: 23045-23154; exon 20: 23795-23895; exon
      21: 23973-24093; exon 22: 24354-24432; exon 23:
      25026-25170; exon 24: 25812-26036; polyadenylation
      signal: 26447-26452

<220>
<221> variation
<222> (826)..(23879)

<223> s at positions 826 and 23180 is G or C; y at
      positions 1914, 5568, 7165, 16431, 1857 and 20486
      is C or T; n at position 13128 is t or tgat; r at
      positions 22211 and 23879 is A or G.

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gcg ctt tgc tcg ctg ctg cgg tcc gcg gcc gga cgc acc atg tcg cag   104
Ala Leu Cys Ser Leu Leu Arg Ser Ala Ala Gly Arg Thr Met Ser Gln
            5   10   15

gga cgc acc ata tcg cag gca ccc gcc cgc cgc gag cgg ccg cgc aag   152
Gly Arg Thr Ile Ser Gln Ala Pro Ala Arg Arg Glu Arg Pro Arg Lys
        20   25   30

gac ccg ctg cgg cac ctg cgc acg cga gag aag cgc gga ccg tcg ggg   200
Asp Pro Leu Arg His Leu Arg Thr Arg Glu Lys Arg Gly Pro Ser Gly
 35   40   45   50

tgc tcc ggc ggc cca aac acc gtg tac ctg cag gtg gtg gca gcg ggt   248
Cys Ser Gly Gly Pro Asn Thr Val Tyr Leu Gln Val Val Ala Ala Gly
                55   60   65

agc cgg gac tcg ggc gcc gcg ctc tac gtc ttc tcc gag ttc aac   293
Ser Arg Asp Ser Gly Ala Ala Leu Tyr Val Phe Ser Glu Phe Asn
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Ser Gln Gly Arg Thr Ile Ser Gln Ala Pro Ala Arg Arg Glu Arg Pro
                20   25   30

Arg Lys Asp Pro Leu Arg His Leu Arg Thr Arg Glu Lys Arg Gly Pro
            35   40   45

Ser Gly Cys Ser Gly Gly Pro Asn Thr Val Tyr Leu Gln Val Val Ala
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Asn



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Ala Leu Arg Ser Leu Leu Arg Pro Leu Gly Leu Arg Thr Met Ser Gln
         5                   10                  15

ggt tcg gct cgt cgg ccg cgg cca ccc aag gac cca ctg cga cac ctg  152
Gly Ser Ala Arg Arg Pro Arg Pro Pro Lys Asp Pro Leu Arg His Leu
     20                  25                  30

cgt acg cgg gag aag cgc ggc ccg ggt ccc ggg ggc ccg aac acc gtg  200
Arg Thr Arg Glu Lys Arg Gly Pro Gly Pro Gly Gly Pro Asn Thr Val
 35                  40                  45                  50

tac ctg cag gtg gtg gcg gcg ggc ggc cgg gac gcg ggg gct gct ctc  248
Tyr Leu Gln Val Val Ala Ala Gly Gly Arg Asp Ala Gly Ala Ala Leu
             55                  60                  65

tat gtc ttc tcg gaa tac aac aggtcagagt gggccgacag ccctggggga     299
Tyr Val Phe Ser Glu Tyr Asn
             70

ttggccccag cgccacgtgc tcgggag                                     326



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<400> 213
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 1               5                   10                  15

Ser Gln Gly Ser Ala Arg Arg Pro Arg Pro Pro Lys Asp Pro Leu Arg
             20                  25                  30

His Leu Arg Thr Arg Glu Lys Arg Gly Pro Gly Pro Gly Gly Pro Asn
         35                  40                  45
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Thr Val Tyr Leu Gln Val Val Ala Ala Gly Gly Arg Asp Ala Gly Ala
    50   55   60

Ala Leu Tyr Val Phe Ser Glu Tyr Asn
65   70